

|        |            |            |            |             |            |            |            |            |
|--------|------------|------------|------------|-------------|------------|------------|------------|------------|
| Heps   | RIVGGRDTSL | GRWPWQVSL. | ....RYDG.A | HLCGGSLLSG  | DWVLTAAHCF | PE....RNRV | LSRWRVFAGA | VAQASPHGLQ |
| Tadg15 | RVVGGTDADE | GEWPWQVSL. | ....HALGQG | HICGASLISP  | NWLVSAAHCF | IDDRGFRYSD | PTQWTAFLGL | HDQSQRSAPG |
| Scce   | KIIDGAPCAR | GSHPWQVAL. | ....LSGNQL | H.CGGVLVNE  | RWVLTAHCF. | .....K     | MNEYTVHLGS | DTLG..DR.R |
| Try    | KIVGGYNCEE | NSVPYQVSL. | ....NSGYHF | ..CGGSLINE  | QWVVSAGHC. | .....Y     | KSRIQVRLGE | HNIEVLEG.N |
| Chymb  | RIVNGEDAVP | GSWPWQVSL. | ....QDKTGF | HFCGGSLISE  | DWVVTAAHC. | .....GV    | RTSDVWVAGE | FDQGSDEE.N |
| Fac7   | RIVGGKVCFK | GECPWQVLL. | ....LVNG.A | QLCGGTLLINT | IKVVSAAHCF | .....AVLGE | HDLSEHDGDE |            |
| Tpa    | RIKGGLFADI | ASHPWQAAIF | AKHRRSPGER | FLCGGILISS  | CWILSAAHCF | QERFPPHHL. | ....TVILGR | .TYRVVFCEE |

|        |            |            |            |            |            |            |             |            |
|--------|------------|------------|------------|------------|------------|------------|-------------|------------|
| Heps   | LGVQAVVYHG | GYLPFRDPNS | EENSNDIALV | HLSS.PLPLT | EYIQPVCLPA | ...AGQALVD | GKICTVTGWG  | NTQYYGQQ.A |
| Tadg15 | VQERRLKRII | SHPPFNDFTF | D...YDIAL  | ELEK.PAEYS | SMVRPICLPD | ...ASHVFPA | GKAIWVTGWG  | HTQYGGTG.A |
| Scce   | AQRIKASKSF | RHPGYSTQT. | ..HVNDMLV  | KLNS.QARLS | SMVKVRLPS  | ...RCE..PP | GTTCTVSGWG  | TTTSPDVTFP |
| Try    | EQFINAAKII | RHPQYDRKT. | ..LNNDIMLI | KLSS.RAVIN | ARVSTISLPT | ...APP..AT | GTKCLISGWG  | NTASSGADYP |
| Chymb  | IQVLKIAKVF | KMPKFSILT. | ..VNNDITLL | KLAT.FARFS | QTVSAVCLPS | ...ADDDFPA | GTLCAATTGWG | KTKYNANKTP |
| Fac7   | QSRRAQVII  | P....STYVP | GTTNHDIAL  | RLHQ.FVVLT | DWVPLCLFE  | RTFSERTLAF | VRFSLVSGWG  | QLDRGATAL  |
| Tpa    | EQKFEVEKYI | VHKEFDDDTY | D...NDIAL  | QLKSDSSRCA | QESSVVRTVC | LPPADLQLPD | WTECELSGYG  | KHEALSPFYS |

|        |            |            |            |            |            |             |            |            |
|--------|------------|------------|------------|------------|------------|-------------|------------|------------|
| Heps   | GVLQEARVPI | ISNDVCNGAD | FYGN..QIKP | KMFCAGYPEG | G.....IDA  | CQGDSSGGPFV | CEDSISRTPR | WRLCGIVSWG |
| Tadg15 | LILQKGEIRV | INQTTCE..N | LLPQ..QITP | RMMCVGFLSG | G.....VDS  | CQGDSSGGPL. | ..SSVEADGR | IFQAGVVSWG |
| Scce   | SDLMCVDVKL | ISPQDCTKV. | .YKD..LLEN | SMLCAGIPDS | K.....KNA  | CNGDSSGGPLV | C....R.... | GTLOGLVSWG |
| Try    | DELQCLDAPV | LSQAKCEAS. | .YPG..KITS | NMFCVGFLEG | G.....KDS  | CQGDSSGGPVV | C....N.... | GQLQGVVSWG |
| Chymb  | DKLQQAALPL | LSNAECKKS. | .WGR..RITD | VMICAG..AS | G.....VSS  | CMGDSSGGPLV | C....QKGA  | WTLVGIVSWG |
| Fac7   | ELMVLNVPR  | MTQDCLQQR  | XVGDSPNITE | YMFCAGYSDG | S.....KDS  | CKGDSSGGP.. | ..HATHYRGT | WYLTGIVSWG |
| Tpa    | ERLKEAHVRL | YPSSRCTSQH | LLNRT..VTD | NMLCAGDTRS | GGPQANLHDA | CQGDSSGGPLV | CLN...DGR  | MTLVGIISWG |

|        |            |            |            |            |               |
|--------|------------|------------|------------|------------|---------------|
| Heps   | T.GCALAQKP | GVYTKVSDFR | EWIFQAIKTH | SEASGWTQL  | (SEQ ID NO:3) |
| Tadg15 | D.GCAQRNKP | GVYTRLPLFR | DWIKENTGV  | -----      | (SEQ ID NO:3) |
| Scce   | TFPCGQPNOP | GVYTQVCKFT | KWINDTMKKH | R-----     | (SEQ ID NO:4) |
| Try    | D.GCAQKNKP | GVYTKVYNYV | KWIKNTIAAN | S-----     | (SEQ ID NO:5) |
| Chymb  | SDTCS.TSSP | GVYARVTCLI | PWVQKILAN  | -----      | (SEQ ID NO:6) |
| Fac7   | Q.GCATVGHF | GVYTRVSQYI | EWLQKLMRSE | PRPGVLLRAP | (SEQ ID NO:7) |
| Tpa    | .LGCGQKDVP | GVYTKVTNYL | DWIRDNMRP  | -----      | (SEQ ID NO:8) |

FIGURE 1

660207-ET212100

66027 E F F 2160

1 TCAAGAGCGGCTCGGGGTACCATGGGAGCGATCGGGCCGCAAGGGCGGAGGGGGCCGAGGAGCTTGGGCGGGGACTCAAGTACAACCTCCGGCAGAGAAAGTGAATGGCTTGA  
M G S D R A R K G G G P K D F G A G L K Y N S R E K V N G L E 33  
121 GGAAGCGGTGGAGTCTCTGCCAGTCAACAAGCTCAAGAAGGTGGAAGAGCATGGCCGGGGCGCTGGGTGGTGTCTGGCAGCGGTGCTGATCGGCTCTCTTGGTCTTCTGGGGATCGG  
E G V E F L P V N N V K K V E K E G P G R W V V L A A V L I G L L L V L L G I G 73  
241 CTCTCTGGTGTGGCATTTCAGTACCGGGAGCTGGTGTCCAGAAAGTCTTCAATGGCTACATGAGGATCACAATGAGAATTTTGGATGCTTACGAGAATCCAACTCCACTGAGTT  
F L V W H L Q Y R D V R V Q K V F N G Y M R I T N E N F V D A Y E N S N S T E F 113  
361 TGTAAAGCTTGGCCAGCAAGGTGAAGGACGGCTGAAGCTGCTGTACAGCGGAGTCCCATCTCTGGGGCCCTACCCAGAGGAGTCCGGCTGTGAGGGCTTCAGCGAGGGCAGCGGTCAATCC  
V S L A S K V K D A L K L L Y S G V P F L G P Y H K E S A V T A F S E G S V I A 153  
481 CTACTACTGGTCTGAGTTTCAGCATCCCGCAGCACCTGGTGGAGGAGCGCGGCGCTCATGGCCGAGGAGCGGGTAGTCATGCTGCCCGCGGGGGCGCTCCCTGAAGTCTCTTGTGGT  
Y Y W S E F S I P Q H L V E E A E R V M A E E R V G V M L P P R A R S L K S F V V 193  
601 CACCTCAGTGGTGGCTTTCCCGCAGGACTCCAAACAGTACAGAGGAGCCAGGACACAGCTGTCAGCTTTGGCTGTCAGCGCCGGGTGTGAGCTGATGGCTTCACGAGCGCGGCTT  
T S V V A F P T D S K T V Q R T Q D N S C S F G L H A R G V E L M R F T T P G F 233  
721 CCCTGACAGCGCTTACCGCTCATGCCCGCTCCAGTGGGCGCTGGGGGGGAGCGGAGCTCAGTGTGAGCGCTCACCTTCCGCACTTTGAGCTTGGCTGTCGAGGAGCGCGGCGAG  
P D S P Y P A H A R C Q W A L R G D A D S V L S L T F R S F D L A S C D E R G S 273  
841 CGAGCTGGTGAAGGTGTACACACCTGAGCGCCATGGAGCGCCAGCGCGCTGGTGCAGTTGTGTGGCACTACCTCCCTCTCTACACCTGAGCTTCCACTCTCCAGAGCTCTCTGT  
D L V T V Y N T L S P M E P H A L V Q L C G T Y P P S Y N L T F H S S Q N V L L 313  
961 CATCACACTGATAACACTGAGCGCGGCTTGGAGCGCACTTCTTCCAGTGGCTAGGATGAGCAGCTGTGGAGCGCGCTTGAAGCGGAGCGGAGCTTCAACAG  
I T L I T N T E R R H P G F E A T F P Q L P R M S S C G G R L R K A Q G G T F N S 353  
1081 CCCTACTACCGAGCGCACTACCCACCAACATTGACTGCACATGGAACATTGAGGTGGCCCAACACCGCATGTGAAGGTGAGCTTCAATCTCTTACTGCTGGAGCGCGCGCTGCC  
P Y Y P G H Y P P H I D C T W N I E V P N N Q H V K V S F K F F Y L L E P G V P 393  
1201 TGGCGGCACTCCCGCAAGGACTACGTGGAGATCAATGGGAGAAATCTCCGAGAGAGGTCCAGCTGGTGGTGGTCCAGCAGCAACAGCAACAGATCAAGTGGCTTCCACTCAGATCA  
A G T C P K D Y V E I N G E K Y C G E R S Q F V V T S N S N K I T V R F E S D Q 433  
1321 GTCTTACCGACCGGCTCTTGAATACCTCTCTTACGATCCAGTACCCATGCCCGGGGAGTTCAAGTCCCGCAGCGGGCGGCTATCCGAGAGGAGCTGGCTGTGATGG  
S Y T D T G F L A E Y L S Y D S S D P C P G Q F T C R T G R C I R K E L R C D G 473  
1441 CTGGCGGAGTGCACCGACCAAGGATGAGCTCAACTGCAGTTGGGAGCGCGGCGCACAGTTCAGCTGCAAGAACAGTTCTGCAAGCGGCTCTCTGGGTGTGCAAGCA  
W A D C T D E S D E L N C S C D A G H Q F T C K N K F C K P L F W V C D S V N D 513  
1561 CTGGGAGACACAGCGAGGAGCGGGGTGAGTGTGCGGCGCCAGAGCTTCAGGTGTTCATGGGAAGTGGCTCTGGAAGCCAGCAGTCAATGGGAAGGAGGAGTGTGGGAGCGG  
C G D N S D E Q G C S C P A Q T F R C S N G K C L S K S Q Q C H G K D D C G D G 553  
1681 GTCCGAGCAGGGCTCTGCGCCCAAGGTGAAGCTCTCTTGTACCAACACACCTACCGCTGGCTCAATGGGCTCTGCTTGAAGGCGCAACCTGAGTGTGAGGGGAGGAGGAGT  
S D E A S C P K V N V V T C T K H T Y R C L N G L C L S K G N P E C D G K E D C 593  
1801 TAGCGAGCGCTCAGATGAGAAGGAGTGGGCTGTGGCTCATCAGGAGACAGGCTGTGTGTGGGGGCGGATGGGATGAGGGGAGTGGGCTGGCAGGTGAAGCTGCA  
S D G S D E K D C D C G L R S F T R Q A R V V G G T D A D E G E W P W Q V S L E 633  
1921 TGCTCTGGGCGAGGCGCACATCTGGGTGCTTCCCTCATCTCTCCCAACTGGCTGGTCTCTGCGGCGACACTGCTACATGATGACAGAGGATTCAAGTACTCAGACCCCGCAGCTGGAC  
A L G Q G H I C G A S L I S P N W L V S A A H C Y I D D R G F R Y S D P T Q W T 673  
2041 GCGCTCTCTGGGCTTGCACAGCAGAGGAGCGCGCGCGCTGGGGTGCAGGAGCGCGAGCTCAAGGCGCATCATCTCCACCGCTTCTTCAATGACTTCACTTGGACTATGACATCG  
A F L G L E D Q S Q R S A P G V Q E R R L K R I I S H P F F N D F T F D Y D I A 713  
2161 GCTGCTGGAGCTGGAGAAACCGGCAGAGTACAGCTCCATGGTGGCGCCATCTGCTGCGGAGCGCTCCCATGTCTTCCCTGCGGCGCAAGGCCACTGGGTCAAGGGCTGGGGACAC  
L L E L E K P A E Y S S M V R P I C L P D A S H V F P A G K A I N V T G W G H T 753  
2281 CCAATATGGAGGAGTGGCGCGCTGATCTGCAAAAGGGTGAGATCCCGCTCATCAACGAGACCACTGCGAGAACCTCTGCGGCGAGGATCAAGCGCGGCTGATGTGGCTGGGCTT  
Q Y G G T G A L I L Q K G E I R V I N Q T T C E N L L P Q Q I T P R M M C V G F 793  
2401 CCTCAGCGCGCGGCTGGAGTCTGCGAGGTGATTCGGGGGAGCCCTGTCCAGCGTGGAGGCGGATGGGGGAGTCTCCAGGCGGCTGTGGTGAAGTGGGAGACGGCTGGCTCAGAG  
L S G G V D S C Q G D S G G P L S S V E A D G R I F Q A G V V S W G D G C A Q R 833  
2521 GAACAAGCCAGCGGTGTACACAGGCTCCCTCTGTTTCGGGACTGGATCAAGAGAACACTGGGGTATAGGGGCGCGGCGCACCAATGTACACTGCGGGCGCACCCATGTGTCAC  
N K P G V Y T R L P L F R D W I K E N T G V (SEQ ID NO: 2) 855  
2641 CCCAGTGTGACCGCTGACGGCTGGAGACTGGACCGCTGACTGCACGAGCGCGCCAGAACATACACTGTGAATCAATTCAGGGGCTCCAAATCTGCTAGAAAACCTCTGCTTCTCT  
2761 CAGCTTCAAGTGGAGCTGGGAGTAGAAGGGAGGAGCACTGGTGGTCTACTGAGCCCACTGGGGGCAAGGTTTGAAGACACAGCTCCCGGCGGAGCGGCGGAGCTGGGGGAGCGG  
2881 CGTTTGTGTATATCTGCTCCCGCTGTGTGAAGGAGCAGCGGAGCGGAGCTTCCGAGCGCTCTGAGTGAAGGTGGTGGGCTGCGGAGCTGCGGCTGTGGGCGCGCTTGGGCGAGCTCT  
3001 TGAGGAAGCCAGGCTGGGAGGAGCTGGAAACAGAGCGGTCTGAGACTGAAATGTTTACCAGCTCCAGGGGTGGAGTTCAGTGTGTGATTTGTGTAATGGGTAAAACATTTAT  
3121 TTCTTTTAAAAA (SEQ ID NO: 1)

FIGURE 2

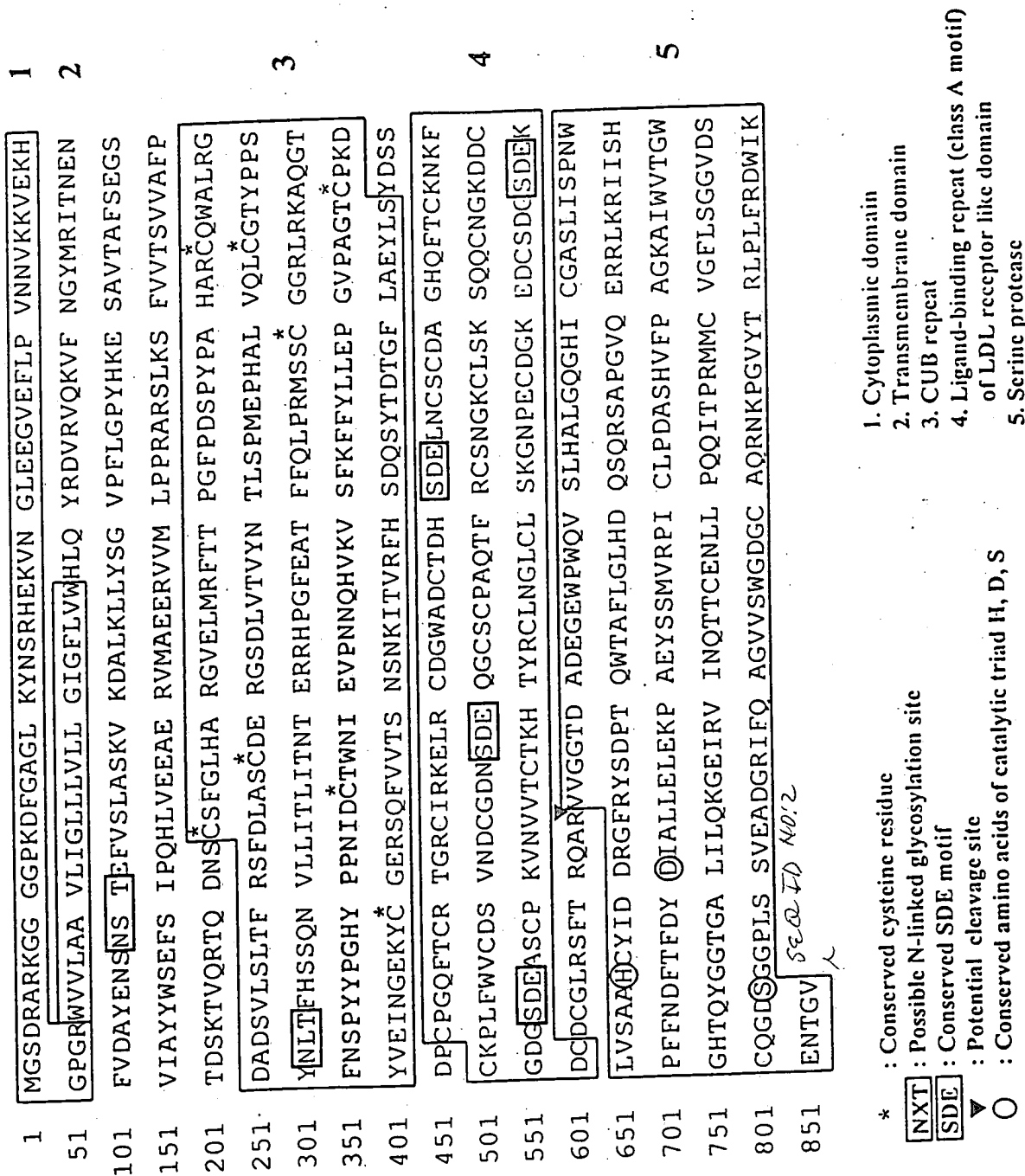


FIGURE 3

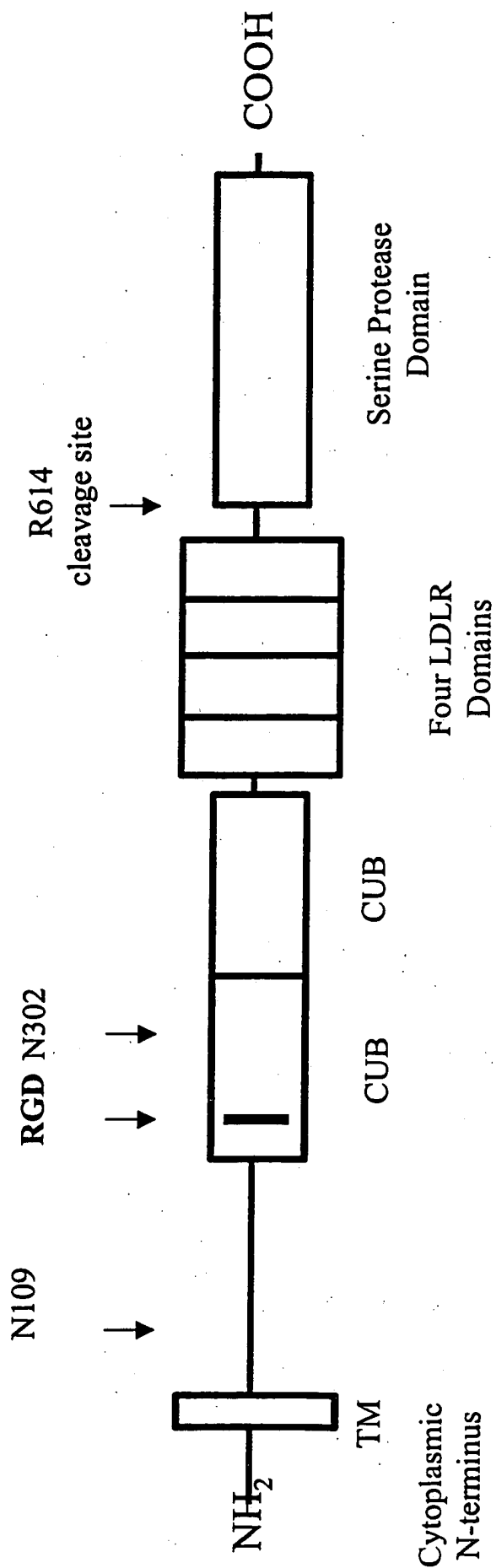


Figure 4

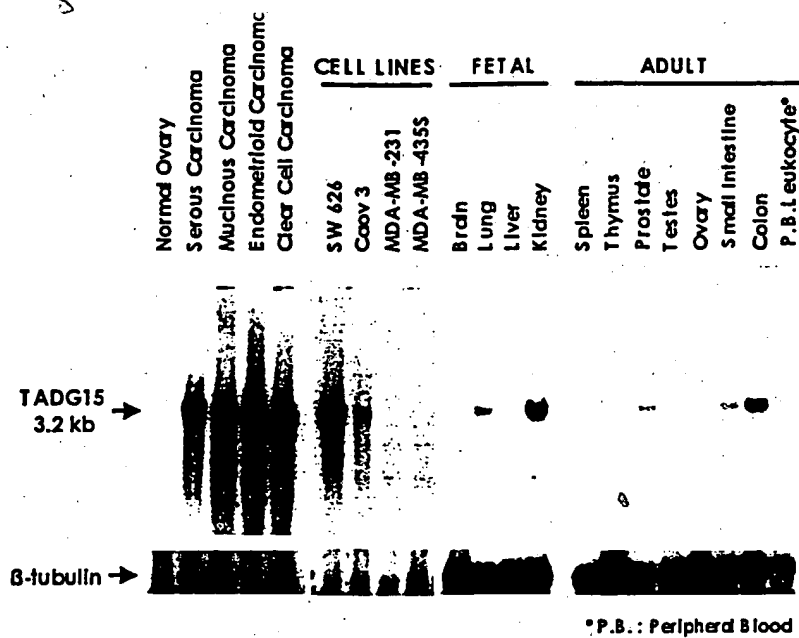
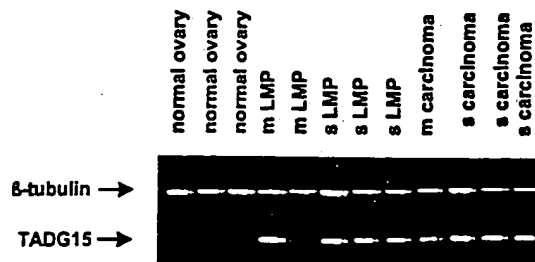


FIGURE 5

A



B

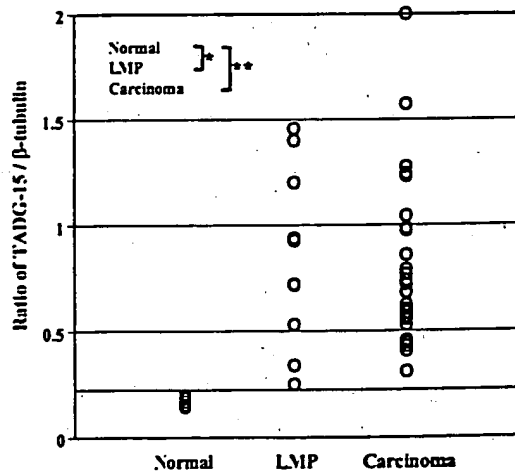


FIGURE 6

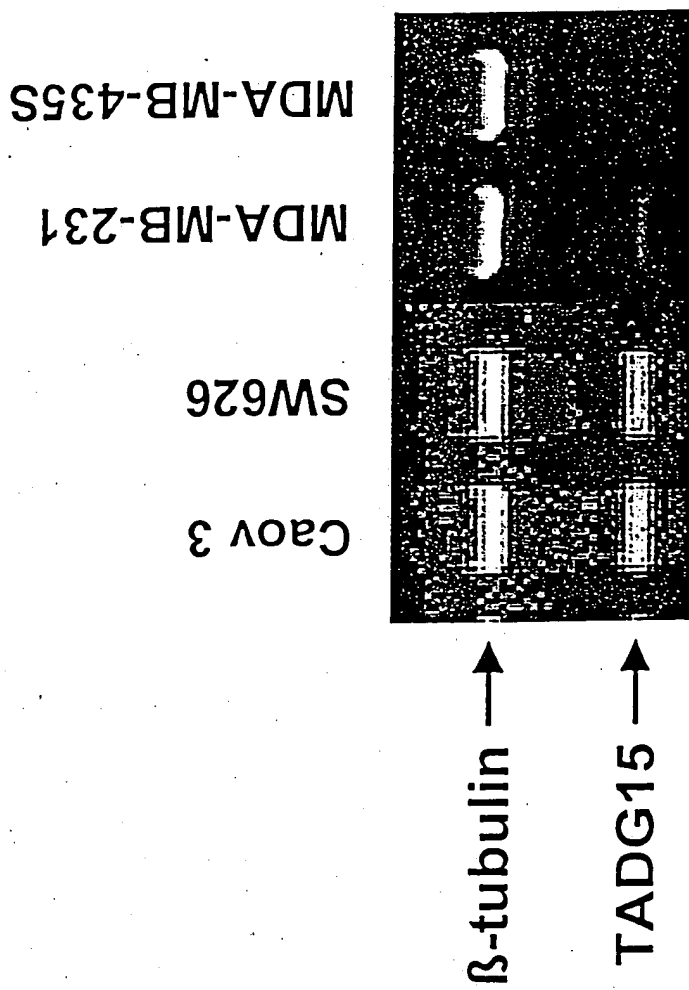


FIGURE 7

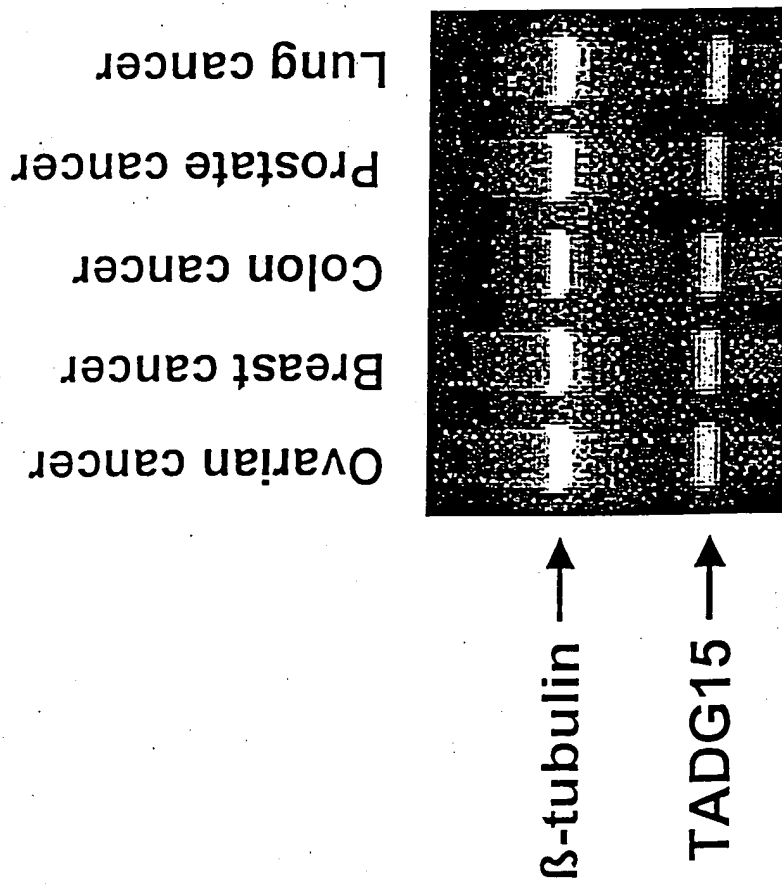


FIGURE 8



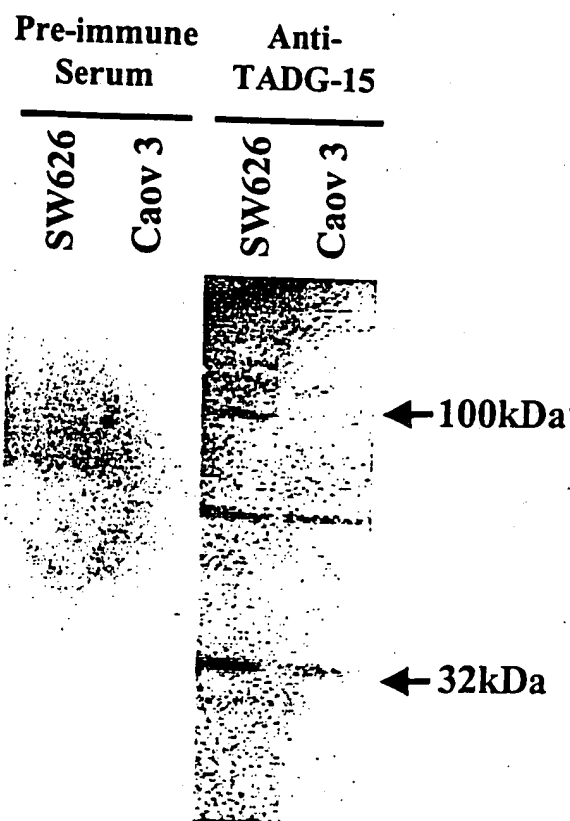


FIGURE 9

660207-E272460

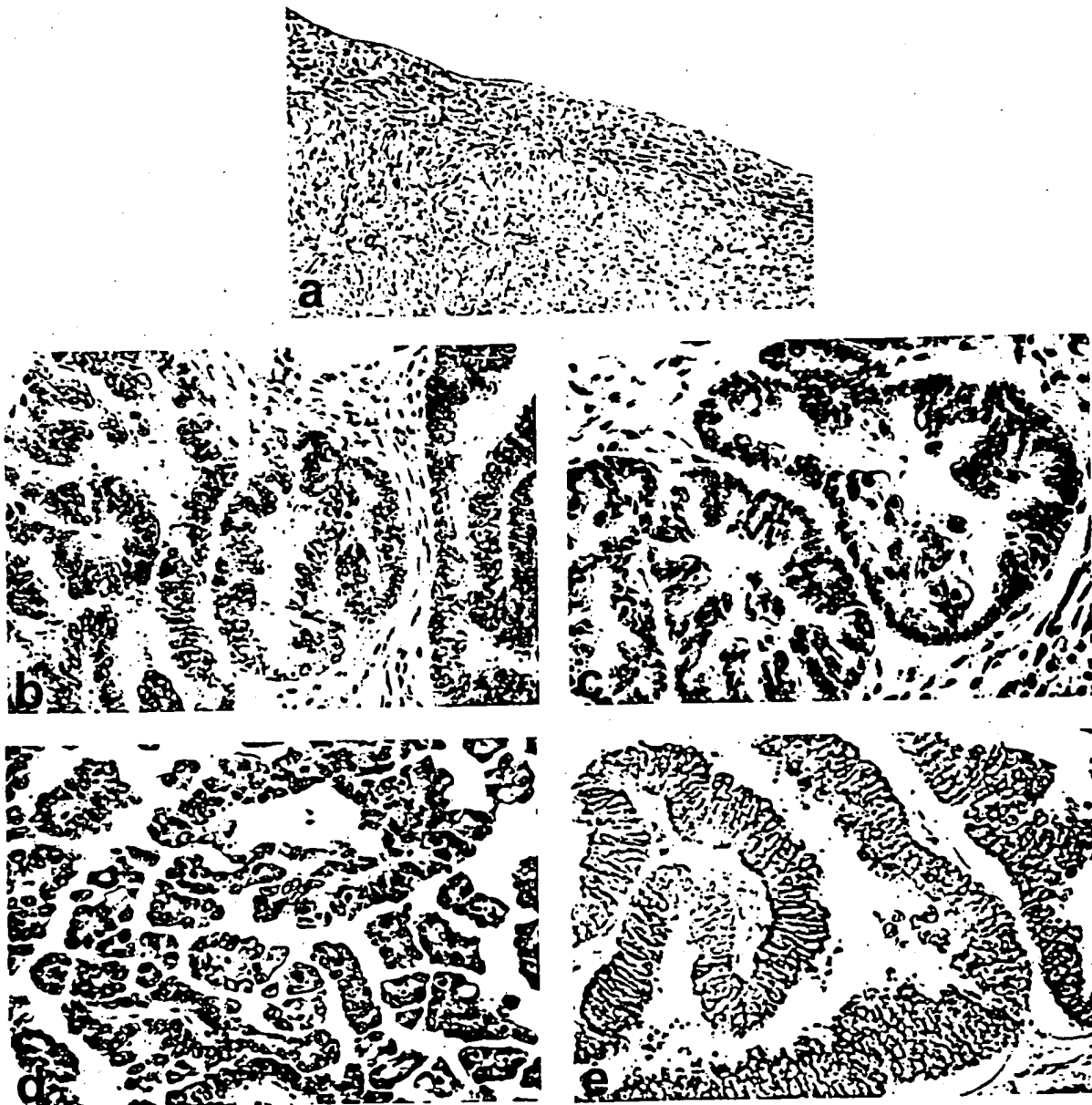


FIGURE 10

66020T ETE400

|          |            |                |            |            |            |     |
|----------|------------|----------------|------------|------------|------------|-----|
| htADG15  | MGSDRARKGG | MDFGAGL        | KYNSRHEKVN | GLEEGVEFL  | VNVKKVEKH  | 50  |
| mEpithin | ---N-G--A- | --SQ-----      | --D--L-NM- | -F-----    | A--A-----R |     |
| htADG15  | GPGRWVVLAA | VLIGLLLVLL     | GIGFLVWHLQ | YRDVRVQKVF | NGYMRITNEN | 100 |
| mEpithin | --R-----V- | --FSF--LS-     | MA-L----FH | --N-----   | --HL-----I |     |
| htADG15  | FVDAYENSNS | TEFVSLASKV     | KDALKLLYSG | VPFLGPHYKE | SAVTAFSEGS | 150 |
| mEpithin | -L-----T-  | ---I---Q-      | -E-----NE  | --V-----K  | -----      |     |
| htADG15  | VIAYYWSEFS | IPQHLVEEAE     | RVMAEERVVM | LPPRARSLSK | FVVTSVVAFP | 200 |
| mEpithin | -----      | --P--A--VD     | -A--V----T | -----A---  | --L-----   |     |
| htADG15  | TDSKTVQRTQ | DNSCSFGLHA     | RGVELMRFTT | PGFPDSPYPA | HARCQWALRG | 250 |
| mEpithin | I-PRML---- | -----A---      | H-AAVT---- | -----N---  | -----V---  |     |
| htADG15  | DADSVLSLTF | RSFDLASCDE     | RGSDLVTVYN | TLSPMEPHAL | VQLCGTYPPS | 300 |
| mEpithin | -----      | -----V-P---    | H-----D    | S-----V    | -R---FS--  |     |
| htADG15  | YNLTFHSSQN | VLLITLITNT     | ERRHPGFEAT | FFQLPRMSSC | GGRLRKAQGT | 350 |
| mEpithin | -----L---- | -F-V-----      | G---L----- | -----K---- | --V-SDT--- |     |
| htADG15  | FNSPYYPGHY | PPNIDCTWNI     | EVPNNQHVKV | SFKFFYLLEP | GVPAGTCPKD | 400 |
| mEpithin | -S-----    | -----N-----    | K---RN---  | R--L---VD- | N--V-S-T-- |     |
| htADG15  | YVEINGEKYC | GERSQFVVT      | NSNKITVRFH | SDQSYTDGTF | LAEYLSYDSS | 450 |
| mEpithin | -----GS    | -----S-        | --S---H--  | --H-----   | -----N     |     |
| htADG15  | DPCPGQFTCR | TGRCIRKELR     | CDGWADCTDH | SDELNCSFDA | GHQFTCKNKF | 500 |
| mEpithin | -----M-M-K | -----          | -----P-Y   | ---RY-R-N- | T-----Q-   |     |
| htADG15  | CKPLFWVCD  | VNDCGDNDE      | QGCSCPAQTF | RCSNGKCLSK | SQQCNGKDDC | 550 |
| mEpithin | -----      | -----G---      | E-----GS-  | K-----PQ   | --K-----N- |     |
| htADG15  | GDGSDEASCP | KVNVVTCTKH     | TYRCINGLCL | SKGNPECDGK | EDCSGDSDEK | 600 |
| mEpithin | -----D     | S---S---Y      | ---Q-----  | -----      | T-----     |     |
| htADG15  | DCDCGLRSFT | RQARVGGTD      | ADEGEWPWQV | SLHALGQGHI | CGASLISPNW | 650 |
| mEpithin | N-----     | K-----N        | -----      | -----L     | -----D-    |     |
| htADG15  | LVSAAHCIYD | DRGFRYSPT      | QWTAFLGLHD | QSQRSAPGVQ | ERRLKRIISH | 700 |
| mEpithin | -----FQ-   | -KN-K---Y-     | M-----L-   | --K---S--- | -LK-----T- |     |
| htADG15  | PFFNDFTFDY | DIALLELEKP     | AEYSSMVRPI | CLPDASHVFP | AGKAIWVTGW | 750 |
| mEpithin | -S-----    | -----S         | V---TV---- | -----T---- | -----      |     |
| htADG15  | GHTQYGGTGA | LILQKGEIRV     | INQTTCEILL | PQITPRMMC  | VGFLSGGVDS | 800 |
| mEpithin | ---KE----- | -----          | -----D-M   | -----      | -----      |     |
| htADG15  | CQGDSSGGLS | SVEADGRIFQ     | AGVVSWDGDC | AQRNKPGVYT | RLPLFRDWIK | 850 |
| mEpithin | -----      | -A-K---M--     | -----E--   | -----      | ---CSSGLDQ |     |
| htADG15  | ENTGV*     | (SEQ ID NO:2)  |            |            |            | 900 |
| mEpithin | RAHWGIAAWT | DSRPQTPTGM     | PDMHTWIER  | NTDDIYAVAS | PPQHNPDCEL |     |
| htADG15  | HP         | (SEQ ID NO:10) |            |            |            | 902 |
| mEpithin | HP         |                |            |            |            |     |

FIGURE 11

LOCUS HSU20428 2900 bp mRNA FRI 17-MAR-1997  
 DEFINITION Human SNC19 mRNA sequence.  
 ACCESSION U20428  
 NID g1890631  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 2900)  
 AUTHORS Zheng, S., Cai, X., Geng, L., Cao, J., Cheng, L. and Zhi, Z.  
 TITLE SNC19 gene in Homo sapiens  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 2900)  
 AUTHORS Zheng, S.  
 TITLE Direct Submission  
 JOURNAL Submitted (30-JAN-1995) Shu Zheng, Cancer Institute, Zhejiang  
 Medical University, Hangzhou, 310003, Peoples Republic of China

TADG15: TCAGAGCGGCTCGGGGTACCATGGGGATCGGGCCCGCAAGGCGGAGGGGGCCCGAGGACTTCGGCGCGGGACT 81

SNC19: .....

82 CAAGTACAACCTCCCGGCACGAGAAAGTGATGGCTTGGAGGAGGGCGTCACTTCTCTGCGAGTCAACACGTCAGAGAGGTGGAAAGCATGGCCCGGG 181

182 CGCTGGGTGGTGTGGCAGCCGTGCTGATCGGCCTCCTCTTGGTCTTGTCTGGGATCGGCTTCTCTGTTGGCATTTCAGTACCGGGACGTGCGTGTCC 281

1 CGCTGGGTGGTGTGGCAGCCGTGCTGATCGGCCTCCTCTTGGTCTTGTCTGGGATCGGCTTCTCTGTTGGCATTTCAGTACCGGGACGTGCGTGTCC 100

282 AGAAGGTCTTCAATGGCTACATGAGGATCACAAATGAGAATTTTGTGATTCCTACGAGTACTCCACTCCACTGAGTTTGTAAAGCCTGGCCAGCAGGT 381

101 AGAAGGTCTTCAATGGCTACATGAGGATCACAAATGAGAATTTTGTGATTCCTACGAGTACTCCACTCCACTGAGTTTGTAAAGCCTGGCCAGCAGGT 200

382 GAGGACCGCGTGAAGCTGCTGTACAGCGGAGTCCATTCTGGGGCCCTTACACAGAGTGTGGGTGTGACGGCCCTTCAGCGAGGGCAGCGTCATCGCC 481

201 GAGGACCGCGTGAAGCTGCTGTACAGCGGAGTCCATTCTGGGGCCCTTACACAGAGTGTGGGTGTGACGGCCCTTCAGCGAGGGCAGCGTCATCGCC 300

482 TACTACTGGTCTGAGTTTACGATCCCGCAGCACCTGGTGGAGGAGGCGGAGCGCGTCATGGCCGAGAGAGCGCGTAGTCATGCTGCCCCCGGGGCGCGCT 581

301 TACTACTGGTCTGAGTTTACGATCCCGCAGCACCTGGTGGAGGAGGCGGAGCGCGTCATGGCCGAGAGAGCGCGTAGTCATGCTGCCCCCGGGGCGCGCT 399

582 CCCTGAAGTCTTTTGTGGTCACTTCAGTGGTGGCTTTCCCGCAGGACTCCAAACAGTACAGAGGACCCAGGACACAGCTGCAGCTTTGGCTTCACGC 681

400 CCCTGAAGTCTTTTGTGGTCACTTCAGTGGTGGCTTTCCCGCAGGACTCCAAACAGTACAGAGGACCCAGGACACAGCTGCAGCTTTGGCTTCACGC 498

682 CCGCGGTGTGGAGCTGATGCGCTTCACACGCGCGGCTTCCTGACAGGCGCTTACCGCGCTCATGCGCGCTGCCAGTGGGCGCTTCGCGGGGGACGCGGAC 781

499 CCGCGGTGTGGAGCTGATGCGCTTCACACG. CCGGCTTCCTGACAGGCGCTTACCGCGCTCATGCGCGCTGCCAGTGGGCGCTTCGCGGGGGACGCGGAC 592

782 TCAGTGTGTGAGCTTACCTTC....CGCAGCTTTGACCTTGGCTCCTTTCAGAGCGCGGCGGACGACCTGGTGAAGGTGTACACACCTGAGCCCCAT 876

593 GCAGTGTGTGAGCTTACCTTCAGCTGAGCTGCGAGC. TTGACTGCGCCT....CGCAGCGCGGCGGACGACCTGGTGAAGGTGTACACACCTGAGCCCCAT 686

877 GGAGCCCCACGCGCTGGTGCAGTTGTGTGGCACCTACCTCCTCTACCTGACCTTCCACT. CCTCCCA. GACGCTCCTGCTCATCACACTGATAA 974

687 GGAGCCCCACG. CTTGGTG. AGTGTGTGGCACCTACCTCCTCTACCTGACCTTCCACTCCTCCCAAGAGCTCCTGCTCATCACACTGATAA 783

975 CCAACACTGAGCGGGCGCATCCCGGCTTTGAGGCCACCTTCTTCAGCTTCCTAGGATGAGCAGCTGTGGAGGCGCGCTTACGTAAAGCCAGGGGACATT 1074

784 CCAACACTGA. CGCGGCATCCCGGCTTTGAGGCCACCTTCTTCAGCTTCCTAGGATGAGCAGCTGTGGAGGCGCGCTTACGTAAAGCCAGGGGACATT 881

1075 CAACAGCCCCCTACTACCCAGGCCACTACCCACCAACATTGACTGCACATGGAACATTGAGGTGCCCAACACCGCATGTGAAGGTGAGCTTCAAATTC 1174

682 CAACAGCCCCCTACTACCCAGGCCACTACCCACCAACATTGACTGCACATGGAACATTGAGGTGCCCAACACCGCATGTGAAGGTGCGCTTCAAATTC 981

1175 TTCTACCTGCTGGAGCCCGCGTGCCTGCGGGCACCTGCCCAAGGACTAGCTGGAGATCAATGGGAGAAATACTGCGGAGAGAGGTCCAGTTTCGTCG 1274

982 TTCTACCTGCTGGAGCCCGCGTGCCTGCGGGCACCTGCCCAAGGACTAGCTGGAGATCAATGGGAGAAATACTGCGGAGAGAGGTCCAGTTTCGTCG 1081

1275 TCACCAGCAACAGCAACAGATCACAGTTTCGCTTCCACTCAGATCAGTCTACACCGACACCGGCTTCTAGCTGAATACCTCTCCTACGACTCCAGTGA 1374

1082 TCACCAGCAACAGCAACAGATCACAGTTTCGCTTCCACTCAGATCAGTCTACACCGACACCGGCTTCTAGCTGAATACCTCTCCTACGACTCCAGTGA 1161

1375 CCCATGCCCGGGGCGATTTCAGTGCACGCGGGCGGTGTATCCGGAAGAGCTGCGCTGTGATGCTGGGCGGACTGCCAGGACACAGCGATGAGCTC 1474

1192 CCCATGCCCGGGGCGATTTCAGTGCACGCGGGCGGTGTATCCGGAAGAGCTGCGCTGTGATGCTGGGCGGACTGCCAGGACACAGCGATGAGCTC 1290

1475 AACTGCAGTTGCGACGCGGGCCACAGTTTCAGTGCAGGAACAGTTTCTGCAAGCCCCCTCTTCTGSGTCTGCGACAGTGTGAACGACTGCGGAGACAACA 1574

1291 AACTGCAGTTGCGACGCGGGCCACAGTTTCAGTGCAGGAACAGTTTCTGCAAG....CTCTTCTGSGTCTGCGACAGTGTGAACGAGTGCAGGAGACAACA 1377

FIGURE 12

1575 GCGACGAGCAAGGGTGCAGTTGTCCGG. CCCAGACCTTCAGGTGTTCCAAATGSSAAGTGCCCTCTCGAAAAGCCAGCAAGTSCAATGGGAAGGACGACTGTG 1673  
 1378 GCGACGAGCAAGGGTGCAGTTGTCCGGACCCAGACCTTCAGGTGTTCCAAATGSSAAGTGCCCTCTCGAAAAGCCAGCAAGTSCAATGGGAAGGACGACTGTG 1477  
 1674 GGGACGGGTCCGACGAGGGCTCCTGCCCAAGGTGAACGTGCTCACTTGACCAACACACCTACCGCTGCCTCAATGSSCTCTGCTTGAGCAAGGGCAA 1773  
 1478 GGGACGGGTCCGACGAGGGCTCCTGCCCAAGGTGAACGTGCTCACTTGACCAACACACCTACCGCTGCCTCAATGSSCTCTGCTTGAGCAAGGGCAA 1577  
 1774 CCCTGAGTGTGACGGGAAGGAGGACTGTAGCGACGGCTCAGATGAGAAGGACTGCGACTGTGGGCTGCGGTCAATCAGCAACAGGGCTCGTGTGTTGGG 1873  
 1578 CCCTGAGTGTGACGGGAAGGAGGACTGTAGCGACGGCTCAGATGAGAAGGACTGCGACTGTGGGCTGCGGTCAATCAGCAACAGGGCTCGTGTGTTGGG 1677  
 1874 GGCACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCTCTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGC 1973  
 1678 GGCACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCTCTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGC 1777  
 1974 TGGTCTCTGCCGCACTGCTACATCGATGACAGAGGATTAGGTACTCAGACCCACGAGTGGACGGCTTCCTGGGCTTGACAGCAGCAGAGCCAGCG 2073  
 1778 TGGTCTCTGCCGCACTGCTACATCGATGACAGAGGATTAGGTACTCAGACCCACGCA. .GGACGGCTTCCTGGGCTTGACAGCAGCAGAGCCAGCG 1875  
 2074 CAGCGCCCTGGGGTGCAGGAGCGCAGGCTCAAGCGCATCATCTCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTGCTGGAGCTG 2173  
 1876 CA. .GGCCCTGGGGTGCAGGAGCGCAGGCTCAAGCGCATCATCTCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTGCTGGAGCTG 1973  
 2174 GAGAAACCGCAGAGTACAGCTCCATGGTGGGCGCCATCTGCCTGCGGACGCTCCCATGTCTTCCCTGCGGCAAGGCTCTGGGTACAGGGCTGGG 2273  
 1974 GAGAAACCGCAGAGTACAGCTCCATGGTGGGCGCCATCTGCCTGCGGACGCTCCCATGTCTTCCCTGCGGCAAGGCTCTGGGTACAGGGCTGGG 2073  
 2274 GACACACCCAGTATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACAGACCCCTGCGAGAACCTCCTGCCGAGCAGAT 2373  
 2074 GACACACCCAGTATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACAGACCCCTGCGAGAACCTCCTGCCGAGCAGAT 2173  
 2374 CACGCCCGCATGATGTGCGTGGGCTTCCCTCAGCGCGCGCTGGACTCCTGCCAGGGTGAATCCGGGGGACCCCTGTCCAGCGTGGAGGGCGGATGGGCGG 2473  
 2174 CACGCCCGCATGATGTGCGTGGGCTTCCCTCAGCGCGCGCTGGACTCCTGCCAGGGTGAATCCGGGGGACCCCTGTCCAGCGTGGAGGGCGGATGGGCGG 2273  
 2474 ATCTTCCAGGCGGTGTGGTGAGCTGGGGAGAGCGGTGCGCTCAGAGGAACAGCCAGGCGGTGTACACAGGCTCCCTCTGTTTGGGACTGGATCAAG 2573  
 2274 ATCTTCCAGGCGGTGTGGTGAGCTGGGGAGAG. GCTGCGCTCAGAGGAACAGCCAGGCGGTGTACACAGGCTCCCTCTGTTTGGGATGGATCAAG 2372  
 2574 AGAACACTGGGGTATAGGGGCGGGGCCACCCAAATGTGTACACCTGCGGGGCCACCCATCGTCCACCCAGTGTGACGCGCTGCAGGCTGGAGACT. . 2670  
 2373 AGAACACTGGGGTATAGGGGCGGGGCCACCCAAATGTGTACACCTGCGGGGCCACCCATCGTCCACCCAGTGTGACGCGCTGCAGGCTGGAGACTCGC 2472  
 2671 GGACCGCTGACTGCACGAGCGCCCCAGAAACATACACTGTGAATCAATCTCCAGGGCTCCAAATCTGCCTAGAAACCTCTCGCTTCTCAGCCTCCAA 2770  
 2473 GCACCGTGACCTGCACGAGCG. CCCAGAAACATACACTGTGAATC. ATCTCCAGG. .CTCAATCTG. CTAGAAACCTCTCGCTTCTCAGCCTCCAA 2567  
 2771 AGTGGAGCTGGGA. GGTAGAAGGGGAGG. AACTGGTGGTTCTACTGACCCACTGGGGGCAAGGTTTGAAGACACAGGCTCCCCCGCCAGCCCCAAGC 2868  
 2568 AGTGGAGCTGGGAGGGTAGAAGGGGAGGAACTGGTGGTTCTACTGACCCACTGGGG. .CAAGGTTTGAAG. CACAG. . .CTCCGGCAGCCC. .AAG 2659  
 2869 TGGGGCAGGCGCGTTTGTGTATATCTGCCCTCCCTGTCTGTAGGAGCAGCGGGAACGGAGCTTCGGAAGCTCCTCACTGAGGTGGTGGGCTGCCGG 2968  
 2659 TGGGGCAGGACGCGTTTGTGCATA. CTGCC. CTGCTCTATACAGGGAAGCTTGA. . . . .TCTCTAGTGA. . . . .GTGTGACTGCCGG 2735  
 2969 ATCTGGGCTGTGGGGCCCTTGGGCCACGCTCTTGAGGAAGCCAGGCTCGGAGGACCTGGAAACAGACGGGTCTGAGACTGAAATGTTTTACCAGCT 3068  
 2736 ATCTGG. . .CTGTGGTCTTGGCCACGCTTCTTGAGGAAGCCAGGCTCGGAGGACCTGGAAACAGACGGGTCTGAGACTGAAATGTTTTACCAGCT 2832  
 3069 CCCAGGGTGGACTTCAGTGTGTATTTGTGTAATGGGTAAACAATTTATTTCTTTTAAAAAAAAAAAAAAAAAAAA 3147 (Seq ID No: 1)  
 2833 CCCAGG. .TGACTTCAGTGTGTGTA. TTGTGTAATGAGTAAACATTTATTTCTTTTAAAAAAAAAAAA. . . . . 2900 (Seq ID No: 9)

12 (continued)  
 FIGURE 12-2